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1/12 FIG. 1

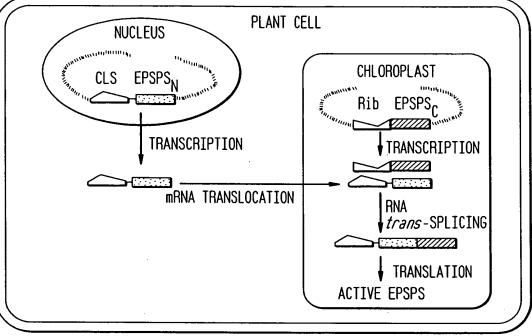
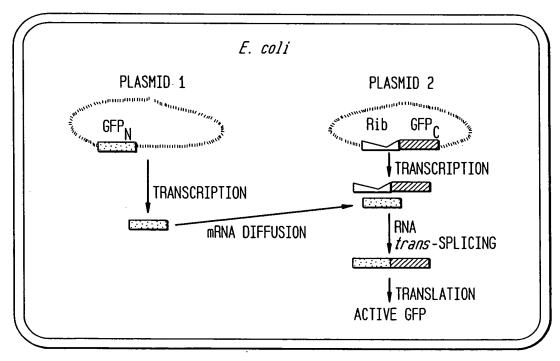


FIG. 2



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FIG. 3

smGFP gene fragment 1 mRNA (SEQ ID NO:2) N N N N N5'..... AUG...... ACAAACAAAAGAAUAGA A CA AGUUAUCAGG U II.II.IIII UCGAUGGUCC G GA TUA CCAAA UUUCUG II IIIII IIII.I AU GGUUU AAAGGC SC C A A GGGAAGA G CÚCUÚCÚ A A U A A C-G G-C U.U C-G *trans-*splicing ribozyme U-A G-C A-U G-C Ã-Ŭ ĀĀ A A U G-U A-UGA U A G I G-GGUA C-G U-A U A G A C smGFP gene fragment 2 mRNA
(SEQ ID NO:1) C-G A-U G-C GACA GAAA GG.GCGU 11 1111 CCACGCA ACUGGG UGGUCC GGAAUCAAAGCUAACUUCAAAAUUAGACACAACAUU.....AAAUAA....3' A C-G UAA ACA G GAUA A j Ä GC

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FIG. 4

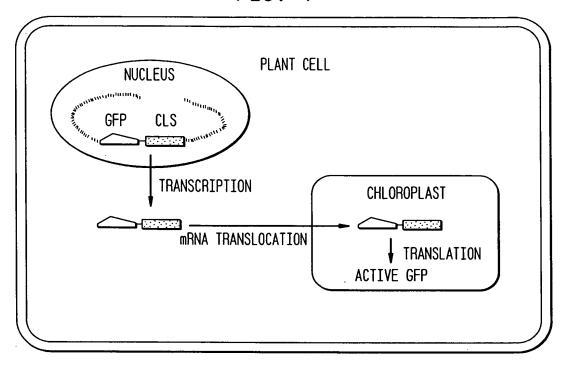


FIG. 5

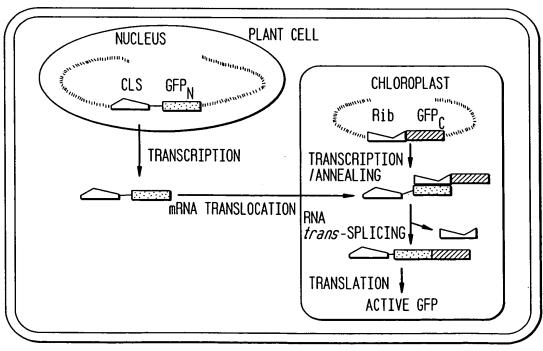


FIG. 6

SEQ ID NO:3

- 1 tttattagaa caagaagtga ggatatgatt aaactttgtt tgacgaaacc
- 51 aggtctgttc cgactttccg actctgagtt tcgacttgtg agagaaggag
- 101 gagtcgtggt gaacttttat taaaaaaatt agttcactcg tcttcaatct
- 151 cttgatcact tcgtctcttc agggaaagat gggaagaaca ctgatgagtc
- 201 tcgcaaggtt tactcctcta tcttcattgt ttttttacaa aatcttg

FIG. 7

5'-	LB	ASBVd(+)	UTR	smGFP	RB	-3'
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FIG. 8A

pVUG1 segment 5689-6757 (SEQ ID NO:4)

5689 tttattagaa caagaagtga ggatatgatt aaactttgtt tgacgaaacc aggtctgttc cgactttccg actctgagtt tcgacttgtg agagaaggag 5739 5789 gagtcgtggt gaacttttat taaaaaaatt agttcactcg tcttcaatct 5839 5889 aataatcaaa cattctgatt agttgataat attagtatta gttggaaatt 5939 ttgtgaaaga ttcctatgaa aagtttcatt aacacggaat tcgtgtcgag 5989 tagaccttgt tgttgtgaga attcttaatt catgagttgt agggagggat 6039 ttATGAGTAA AGGAGAAGAA CTTTTCACTG GAGTTGTCCC AATTCTTGTT 6089 GAATTAGATG GTGATGTTAA TGGGCACAAA TTTTCTGTCA GTGGAGAGGG 6139 TGAAGGTGAT GCAACATACG GAAAACTTAC CCTTAAATTT ATTTGCACTA 6189 CTGGAAAACT ACCTGTTCCA TGGCCAACAC TTGTCACTAC TTTCTCTTAT 6239 GGTGTTCAAT GCTTTTCAAG ATACCCAGAT CATATGAAGC GGCACGACTT 6289 CTTCAAGAGC GCCATGCCTG AGGGATACGT GCAGGAGAGG ACCATCTCTT 6339 TCAAGGACGA CGGGAACTAC AAGACACGTG CTGAAGTCAA GTTTGAGGGA 6389 GACACCCTCG TCAACAGGAT CGAGCTTAAG GGAATCGATT TCAAGGAGGA 6439 CGGAAACATC CTCGGCCACA AGTTGGAATA CAACTACAAC TCCCACAACG 6489 TATACATCAC GGCAGACAAA CAAAAGAATG GAATCAAAGC TAACTTCAAA 6539 ATTAGACACA ACATTGAAGA TGGAAGCGTT CAACTAGCAG ACCATTATCA 6589 ACAAAATACT CCAATTGGCG ATGGCCCTGT CCTTTTACCA GACAACCATT 6639 ACCTGTCCAC ACAATCTGCC CTTTCGAAAG ATCCCAACGA AAAGAGAGAC 6689 CACATGGTCC TTCTTGAGTT TGTAACAGCT GCTGGGATTA CACATGGCAT 6739 GGATGAACTA TACAAATAA

FIG. 8B

pVUG2 segment 5689-6757 (SEQ ID NO:5)

5689 acttgtgaga gaaggaggag tcgtggtgaa cttttattaa aaaaattagt 5739 tcactcgtct tcaatctctt gatcacttcg tctcttcagg gaaagatggg 5789 aagaacactg atgagtctcg caaggtttac tcctctatct tcattgtttt 5839 5889 aataatcaaa cattotgatt agttgataat attagtatta gttggaaatt 5939 ttgtgaaaga ttcctatgaa aagtttcatt aacacggaat tcgtgtcgag 5989 tagaccttgt tgttgtgaga attcttaatt catgagttgt agggagggat 6039 ttatgagtaa aggagaagaa ciiitcactg gagiigiccc aaticiigii 6089 GAATTAGATG GTGATGTTAA TGGGCACAAA TTTTCTGTCA GTGGAGAGGG 6139 TGAAGGTGAT GCAACATACG GAAAACTTAC CCTTAAATTT ATTTGCACTA 6189 CTGGAAAACT ACCTGTTCCA TGGCCAACAC TTGTCACTAC TTTCTCTTAT 6239 GGTGTTCAAT GCTTTTCAAG ATACCCAGAT CATATGAAGC GGCACGACTT 6289 CTTCAAGAGC GCCATGCCTG AGGGATACGT GCAGGAGAGG ACCATCTCTT 6339 TCAAGGACGA CGGGAACTAC AAGACACGTG CTGAAGTCAA GTTTGAGGGA 6389 GACACCCTCG TCAACAGGAT CGAGCTTAAG GGAATCGATT TCAAGGAGGA 6439 CGGAAACATC CTCGGCCACA AGTTGGAATA CAACTACAAC TCCCACAACG 6489 TATACATCAC GGCAGACAAA CAAAAGAATG GAATCAAAGC TAACTTCAAA 6539 ATTAGACACA ACATTGAAGA TGGAAGCGTT CAACTAGCAG ACCATTATCA 6589 ACAAAATACT CCAATTGGCG ATGGCCCTGT CCTTTTACCA GACAACCATT 6639 ACCTGTCCAC ACAATCTGCC CTTTCGAAAG ATCCCAACGA AAAGAGAGAC 6689 CACATGGTCC TTCTTGAGTT TGTAACAGCT GCTGGGATTA CACATGGCAT 6739 GGATGAACTA TACAAATAA

FIG. 8C

pVUG3 segment 6833-7901 (SEQ ID NO:6)

6833 tcttcaggga aagatgggaa gaacactgat gagtctcgca aggtttactc 6883 ctctatcttc attgtttttt tacaaaatct tgtttattag aacaagaagt 6933 gaggatatga ttaaactttg tttgacgaaa ccaggtctgt tccgactttc 6983 cgactotgag tttcgctagc atgtatttgg caaatcaaat accatggtct 7033 aataatcaaa cattotgatt agttgataat attagtatta gttggaaatt 7083 ttgtgaaaga ttcctatgaa aagtttcatt aacacggaat tcgtgtcgag 7133 tagaccttgt tgttgtgaga attcttaatt catgagttgt agggagggat 7183 ttatgagtaa aggagaagaa cttttcactg gagttgtccc aattcttgtt 7233 GAATTAGATG GTGATGTTAA TGGGCACAAA TTTTCTGTCA GTGGAGAGGG 7283 TGAAGGTGAT GCAACATACG GAAAACTTAC CCTTAAATTT ATTTGCACTA 7333 CTGGAAAACT ACCTGTTCCA TGGCCAACAC TTGTCACTAC TTTCTCTTAT 7383 GGTGTTCAAT GCTTTTCAAG ATACCCAGAT CATATGAAGC GGCACGACTT 7433 CTTCAAGAGC GCCATGCCTG AGGGATACGT GCAGGAGAGG ACCATCTCTT 7483 TCAAGGACGA CGGGAACTAC AAGACACGTG CTGAAGTCAA GTTTGAGGGA 7533 GACACCCTCG TCAACAGGAT CGAGCTTAAG GGAATCGATT TCAAGGAGGA 7583 CGGAAACATC CTCGGCCACA AGTTGGAATA CAACTACAAC TCCCACAACG 7633 TATACATCAC GGCAGACAAA CAAAAGAATG GAATCAAAGC TAACTTCAAA 7683 ATTAGACACA ACATTGAAGA TGGAAGCGTT CAACTAGCAG ACCATTATCA 7733 ACAAAATACT CCAATTGGCG ATGGCCCTGT CCTTTTACCA GACAACCATT 7783 ACCTGTCCAC ACAATCTGCC CTTTCGAAAG ATCCCAACGA AAAGAGAGAC 7833 CACATGGTCC TTCTTGAGTT TGTAACAGCT GCTGGGATTA CACATGGCAT 7883 GGATGAACTA TACAAATAA

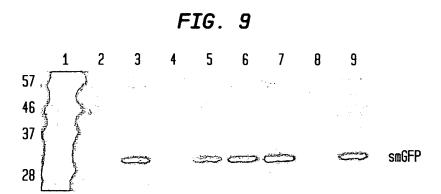
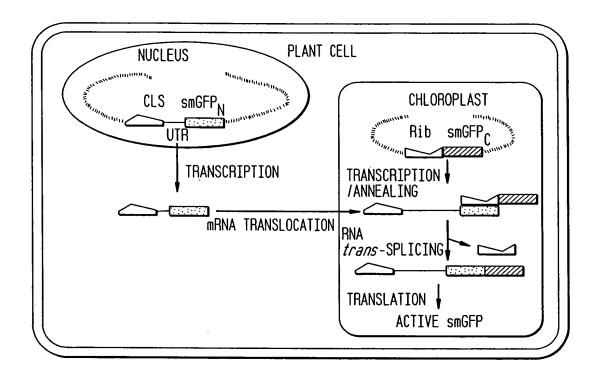


FIG. 10



10/12 FIG. 11A

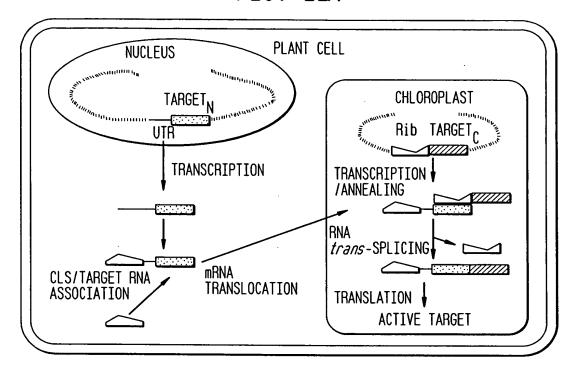
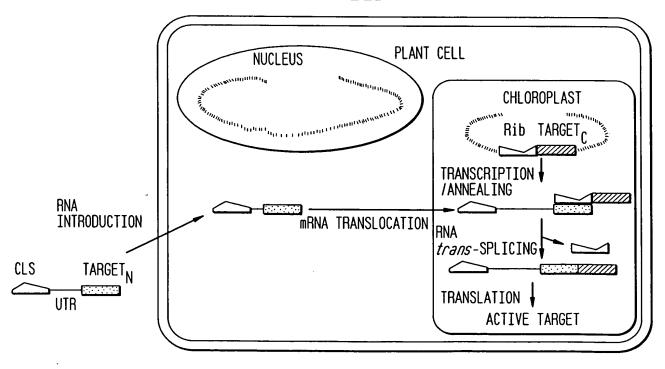


FIG. 11B



11/12 FIG. 11C

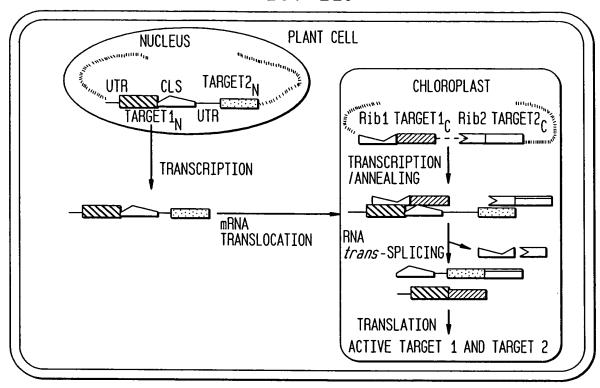
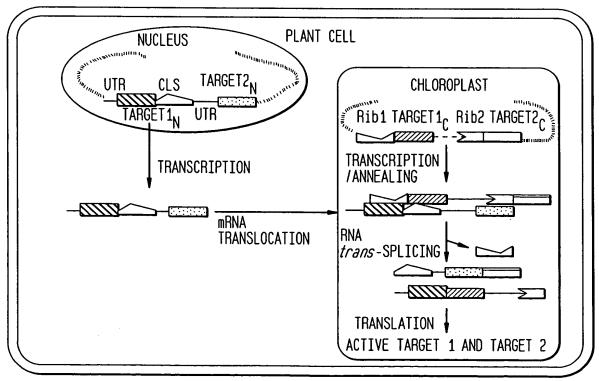


FIG. 11D



12/12 FIG. 11E

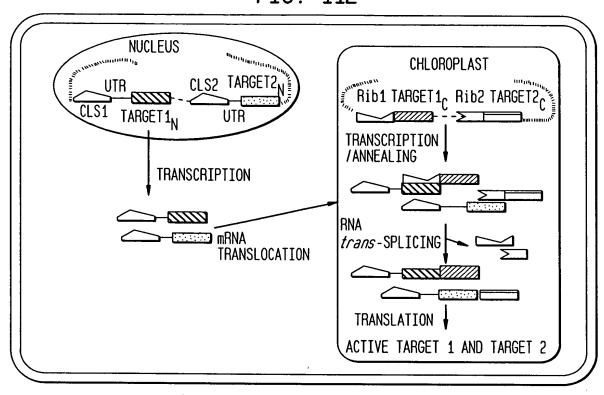


FIG. 11F

